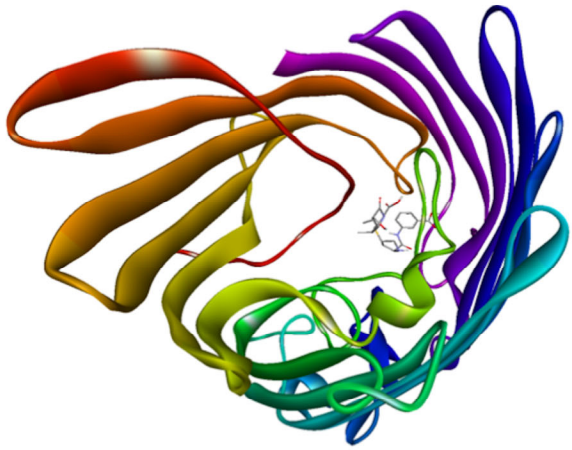
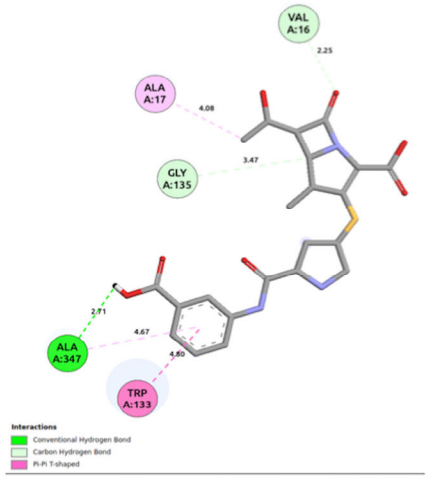
Homology Modeling and Molecular Dockings for *K. pneumoniae*

(A) Ligand Docking, Ertapenem

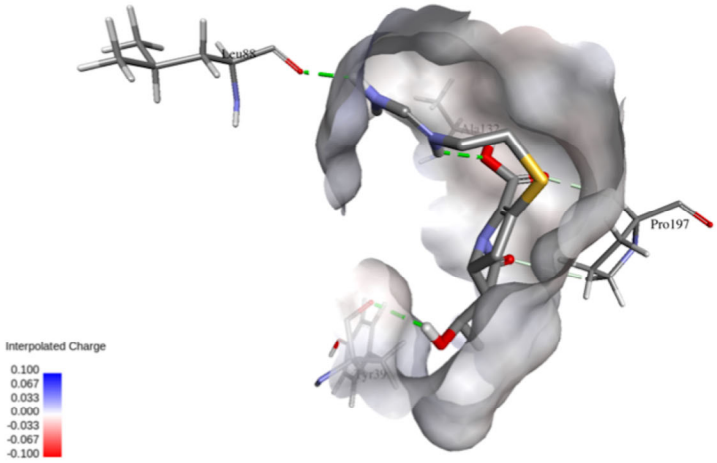


(B) 2D Interaction Model, Ertapenem

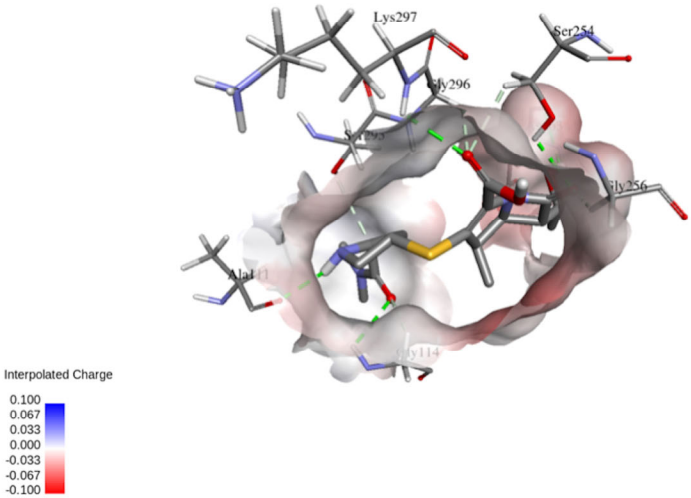


(C) Receptor-Ligand Complex, Imipenem

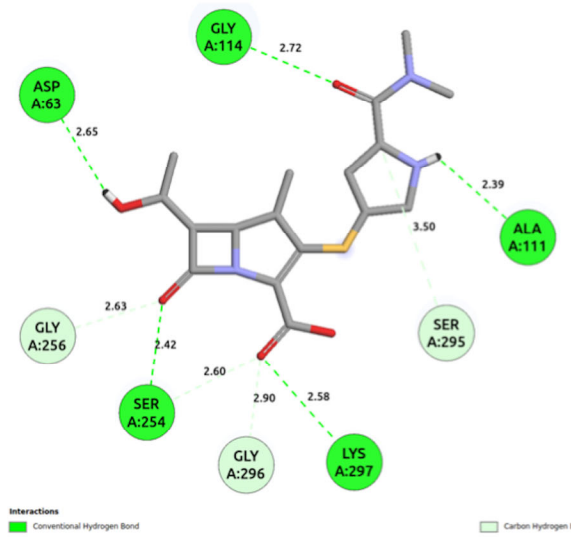
(D) Pocket Interaction, Imipenem



(E) Pocket Interaction, Meropenem



(F) 2D Interaction Model, Meorpenem



Supplementary Figure 6. Homology modeling docking of novel AMR genes predicted for *K. pneumoniae* for antibiotics (Ertapenem, Imipenem, and Meropenem). **6a.** Receptor (WP_049116479.1) and ligand (Ertapenem) complex. **6b.** 2D interaction model for receptor (WP_049116479.1) and ligand (Ertapenem). **6c.** Receptor (WP_064146913.1) and ligand (Imipenem) complex. **6d.** Pocket interaction for receptor (WP_064146913.1) and ligand (Imipenem). **6e.** Pocket Interaction for receptor (WP_125961907.1) and ligand (Meropenem). **6f** 2D Interaction Model for receptor (WP_125961907.1) and ligand (Meropenem).